

<110> Karunanandaa, Balasulojini
 Yu, Jaehyuk
 Kishore, Ganesh M.

<120> NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
 WITH STEROL SYNTHESIS AND METABOLISM

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<150> US 60/142,981

<151> 1999-07-12

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atg gag tac tct tac ctg tta gat atg gcg gac aag act gag gat cca 101
 Met Glu Tyr Ser Tyr Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro
 15 20 25

tac atg aga cta gta tat gct tca tca ttc ttt ata tct gtc tac tat 149
 Tyr Met Arg Leu Val Tyr Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr
 30 35 40

gcc tat caa cga acg tgg aag cca ttc aat cca att ctt ggt gag act 197
 Ala Tyr Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr
 45 50 55

tat gaa atg gtt aac cat ggt ggc att aca ttt ata tca gag cag gtc 245
 Tyr Glu Met Val Asn His Gly Gly Ile Thr Phe Ile Ser Glu Gln Val
 60 65 70

agt cat cac cct cca atg agt gct ggg cat gct gaa act gaa cat ttc 293
 Ser His His Pro Pro Met Ser Ala Gly His Ala Glu Thr Glu His Phe
 75 80 85 90

act tat gat gtt aca tca aaa ttg aaa acc aaa ttt ctc ggc aac tca 341
 Thr Tyr Asp Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser
 95 100 105

gtt gat gta tat cct gtt gga aga acg cgt gtt acc ctc aaa aga gat 389
 Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp
 110 115 120

| | |
|---|------|
| ggt gtg gtc ctt gat ttg gtg cct cct cct aca aaa gtt agc aac ttg | 437 |
| Gly Val Val Leu Asp Leu Val Pro Pro Pro Thr Lys Val Ser Asn Leu | |
| 125 130 135 | |
| att ttt gga cga act tgg att gat tca cca gga gag atg atc ctg aca | 485 |
| Ile Phe Gly Arg Thr Trp Ile Asp Ser Pro Gly Glu Met Ile Leu Thr | |
| 140 145 150 | |
| aat ctg act aca ggg gac aaa gtg gtg ctg tat ttt caa cca tgt ggc | 533 |
| Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly | |
| 155 160 165 170 | |
| tgg ttt gga tat gaa gtg gat ggg tac gtg tat aat tct gct gac gag | 581 |
| Trp Phe Gly Tyr Glu Val Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu | |
| 175 180 185 | |
| cct aag ata ctg atg act gga aaa tgg aat gag gct atg aat tat caa | 629 |
| Pro Lys Ile Leu Met Thr Gly Lys Trp Asn Glu Ala Met Asn Tyr Gln | |
| 190 195 200 | |
| gtt tgt gac tca gag gga gaa cca ctt cca ggc act gag ttg aaa gag | 677 |
| Val Cys Asp Ser Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu | |
| 205 210 215 | |
| att tgg aga gtt gct gat acc ccg aag aag gac aag ttc cag tac acg | 725 |
| Ile Trp Arg Val Ala Asp Thr Pro Lys Lys Asp Lys Phe Gln Tyr Thr | |
| 220 225 230 | |
| cat ttt gca cac aag att aac agc ttt gac act gct ccc aag aag ttg | 773 |
| His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu | |
| 235 240 245 250 | |
| ttg gca tct gac tct cgt cta cgt cct gat aga atg gcc ctt gag aag | 821 |
| Leu Ala Ser Asp Ser Arg Leu Arg Pro Asp Arg Met Ala Leu Glu Lys | |
| 255 260 265 | |
| ggt gac cta tcc aca tct ggt tat gag aag agc agt ttg gag gag agg | 869 |
| Gly Asp Leu Ser Thr Ser Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg | |
| 270 275 280 | |
| caa aga gct gag aag aga aac cga gag gcc aag ggc cat aag ttc act | 917 |
| Gln Arg Ala Glu Lys Arg Asn Arg Glu Ala Lys Gly His Lys Phe Thr | |
| 285 290 295 | |
| cct aga tgg ttt gat tta aca gat gaa gta act cct acc cct tgg ggt | 965 |
| Pro Arg Trp Phe Asp Leu Thr Asp Glu Val Thr Pro Thr Pro Trp Gly | |
| 300 305 310 | |
| gac ttg gaa gtt tac caa tac aac ggt aaa tat acc caa cat tgt gct | 1013 |
| Asp Leu Glu Val Tyr Gln Tyr Asn Gly Lys Tyr Thr Gln His Cys Ala | |
| 315 320 325 330 | |
| gcc gtt gat agt tct gag tgc att gaa gtg cct gac atc aga cca gaa | 1061 |
| Ala Val Asp Ser Ser Glu Cys Ile Glu Val Pro Asp Ile Arg Pro Glu | |
| 335 340 345 | |

20E240-LE50E00T

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ttc aac cct tgg caa tat gat aat ttg gat gct gaa tag tgagcatcct      1110
Phe Asn Pro Trp Gln Tyr Asp Asn Leu Asp Ala Glu
      350                      355

tgtggaattc tttctatattt ttttaaatat cattttgtta ttaagtttgt aatgtaatct  1170

tgattggaat gcttgaaatt tggttttgtt tttgggttgt tttatcactg tagtatttga  1230

ttaattaata gtagctatgt tagttcatca gttcactttg catggataaa tgctagtagg  1290

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          Met Cys Asn Asn Gly Gln Ser Pro Leu Asp Arg Phe Ile
            1              5              10

tct gtg gta gca tgg tgc ata tct acc act cgc cct gtg act ttt ggt      159
Ser Val Val Ala Trp Cys Ile Ser Thr Thr Arg Pro Val Thr Phe Gly
      15              20              25

gtt gct cct tat aat ccc att ctt ggt gag aca cac cat gtt tca agg      207
Val Ala Pro Tyr Asn Pro Ile Leu Gly Glu Thr His His Val Ser Arg
      30              35              40              45

gga aat ctt aat gtg tta ttg gag cag att tca cat cac cct cca gta      255
Gly Asn Leu Asn Val Leu Leu Glu Gln Ile Ser His His Pro Pro Val
            50              55              60

act gct ctc cat gca aca gat gag aag gaa aac att gaa atg tta tgg      303
Thr Ala Leu His Ala Thr Asp Glu Lys Glu Asn Ile Glu Met Leu Trp
            65              70              75

tgc cag cga cct gat cca aag ttt aat ggc aca tca gtt gaa gct aaa      351
Cys Gln Arg Pro Asp Pro Lys Phe Asn Gly Thr Ser Val Glu Ala Lys
            80              85              90

gtg cat gga ata cgc cag ttg aag ctc cta aat cat ggt gaa aca tat      399
Val His Gly Ile Arg Gln Leu Lys Leu Leu Asn His Gly Glu Thr Tyr
            95              100              105

gaa atg aat tgt cct cgc ctt tta ctt aga att ctt cca gtt cct ggt      447

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| | |
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| Glu Met Asn Cys Pro Arg Leu Leu Leu Arg Ile Leu Pro Val Pro Gly | |
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| gct gat tgg gct ggt aca gtt aat ata cgg tgc cta gag aca ggt cta | 495 |
| Ala Asp Trp Ala Gly Thr Val Asn Ile Arg Cys Leu Glu Thr Gly Leu | |
| 130 135 140 | |
| gta gct gaa tta tcc tac aga tca agt tct ttt cta gga att ggg ggg | 543 |
| Val Ala Glu Leu Ser Tyr Arg Ser Ser Ser Phe Leu Gly Ile Gly Gly | |
| 145 150 155 | |
| aat cat aga gtg atc aaa ggg aag atc ctt gac tct tca tca ttg aaa | 591 |
| Asn His Arg Val Ile Lys Gly Lys Ile Leu Asp Ser Ser Ser Leu Lys | |
| 160 165 170 | |
| gtt cta tat gaa gtt gat ggt cat tgg gat agg acc gta aaa gtg aag | 639 |
| Val Leu Tyr Glu Val Asp Gly His Trp Asp Arg Thr Val Lys Val Lys | |
| 175 180 185 | |
| gac aca aat aat ggg aaa gta aga gtg ata tat gat gca aag gaa gtt | 687 |
| Asp Thr Asn Asn Gly Lys Val Arg Val Ile Tyr Asp Ala Lys Glu Val | |
| 190 195 200 205 | |
| atg tca ggt ctc gaa act cct ata ctc aag gac ata gag ggt gtg tgg | 735 |
| Met Ser Gly Leu Glu Thr Pro Ile Leu Lys Asp Ile Glu Gly Val Trp | |
| 210 215 220 | |
| caa aca gaa tca gct cat gtt tgg ggt gaa tta aac caa gcc att gtg | 783 |
| Gln Thr Glu Ser Ala His Val Trp Gly Glu Leu Asn Gln Ala Ile Val | |
| 225 230 235 | |
| agc aaa gac tgg gag aaa gca aga gaa gca aag cta aaa gtt gag gaa | 831 |
| Ser Lys Asp Trp Glu Lys Ala Arg Glu Ala Lys Leu Lys Val Glu Glu | |
| 240 245 250 | |
| aga caa agg gag ctt gtg aga gaa aga gaa tca aaa gga gaa aca tgg | 879 |
| Arg Gln Arg Glu Leu Val Arg Glu Arg Glu Ser Lys Gly Glu Thr Trp | |
| 255 260 265 | |
| att tct aag cat ttt gta gtt tct aac aac aaa gaa ggg tgg caa tgt | 927 |
| Ile Ser Lys His Phe Val Val Ser Asn Asn Lys Glu Gly Trp Gln Cys | |
| 270 275 280 285 | |
| tca cct att cat aag agt gta cct gcg gcc ccc atc aca gcc cta taa | 975 |
| Ser Pro Ile His Lys Ser Val Pro Ala Ala Pro Ile Thr Ala Leu | |
| 290 295 300 | |
| ttgttgtcac tgtcaagtag tgtaaagcat taaagtacat tttagaagag aatgttcata | 1035 |
| aaaaaattta atggttgaaa ttttgacaac aatgaagtat ataacaaaat ttaaaattag | 1095 |
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Ser Tyr Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Met Arg
      10                      15                      20

cta gta tat gct tca tca ttc ttt ata tct gtc tac tat gcc tat caa      148
Leu Val Tyr Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr Ala Tyr Gln
      25                      30                      35

cga acg tgg aag cca ttc aat cca att ctt ggt gag act tat gaa atg      196
Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu Met
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gtt aac cat ggt ggc att aca ttt ata tca gag cag gtc agt cat cac      244
Val Asn His Gly Gly Ile Thr Phe Ile Ser Glu Gln Val Ser His His
      60                      65                      70

cct cca atg agt gct ggg cat gct gaa act gaa cat ttc act tat gat      292
Pro Pro Met Ser Ala Gly His Ala Glu Thr Glu His Phe Thr Tyr Asp
      75                      80                      85

gtt aca tca aaa ttg aaa acc aaa ttt ctc ggc aac tca gtt gat gta      340
Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Val Asp Val
      90                      95                      100

tat cct gtt gga aga acg cgt gtt acc ctc aaa aga gat ggt gtg gtc      388
Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val Val
      105                      110                      115

ctt gat ttg gtg cct cct cct aca aaa gtt agc aac ttg att ttt gga      436
Leu Asp Leu Val Pro Pro Pro Thr Lys Val Ser Asn Leu Ile Phe Gly
      120                      125                      130                      135

cga act tgg att gat tca cca gga gag atg atc ctg aca aat ctg act      484
Arg Thr Trp Ile Asp Ser Pro Gly Glu Met Ile Leu Thr Asn Leu Thr
      140                      145                      150

aca ggg gac aaa gtg gtg ctg tat ttt caa cca tgt ggc tgg ttt gga      532
Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe Gly
      155                      160                      165

gct ggt aga tat gaa gtg gat ggg tac gtg tat aat tct gct gac gag      580
Ala Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu
      170                      175                      180

cct aag ata ctg atg act gga aaa tgg aat gag gct atg aat tat caa      628

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| | | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|------------|-----|-----|------|--|
| Pro | Lys | Ile | Leu | Met | Thr | Gly | Lys | Trp | Asn | Glu | Ala | Met | Asn | Tyr | Gln | | |
| 185 | | | | | | 190 | | | | | 195 | | | | | | |
| gtt | tgt | gac | tca | gag | gga | gaa | cca | ctt | cca | ggc | act | gag | ttg | aaa | gag | 676 | |
| Val | Cys | Asp | Ser | Glu | Gly | Glu | Pro | Leu | Pro | Gly | Thr | Glu | Leu | Lys | Glu | | |
| 200 | | | | | 205 | | | | | 210 | | | | | 215 | | |
| att | tgg | aga | gtt | gct | gat | acc | ccg | aag | aag | gac | aag | ttc | cag | tac | acg | 724 | |
| Ile | Trp | Arg | Val | Ala | Asp | Thr | Pro | Lys | Lys | Asp | Lys | Phe | Gln | Tyr | Thr | | |
| | | | | 220 | | | | | | 225 | | | | 230 | | | |
| cat | ttt | gca | cac | aag | att | aac | agc | ttt | gac | act | gct | ccc | aag | aag | ttg | 772 | |
| His | Phe | Ala | His | Lys | Ile | Asn | Ser | Phe | Asp | Thr | Ala | Pro | Lys | Lys | Leu | | |
| | | | | 235 | | | | 240 | | | | | 245 | | | | |
| ttg | gca | tct | gac | tct | cgt | cta | cgt | cct | gat | aga | atg | gcc | ctt | gag | aag | 820 | |
| Leu | Ala | Ser | Asp | Ser | Arg | Leu | Arg | Pro | Asp | Arg | Met | Ala | Leu | Glu | Lys | | |
| | | 250 | | | | | 255 | | | | | 260 | | | | | |
| ggt | gac | cta | tcc | aca | tct | ggt | tat | gag | aag | agc | agt | ttg | gag | gag | agg | 868 | |
| Gly | Asp | Leu | Ser | Thr | Ser | Gly | Tyr | Glu | Lys | Ser | Ser | Leu | Glu | Glu | Arg | | |
| | 265 | | | | | 270 | | | | | 275 | | | | | | |
| caa | aga | gct | gag | aag | aga | aac | cga | gag | gcc | aag | ggc | cat | aag | ttc | act | 916 | |
| Gln | Arg | Ala | Glu | Lys | Arg | Asn | Arg | Glu | Ala | Lys | Gly | His | Lys | Phe | Thr | | |
| 280 | | | | | 285 | | | | | 290 | | | | | 295 | | |
| cct | aga | tgg | ttt | gat | tta | aca | gat | gaa | gta | act | cct | acc | cct | tgg | ggt | 964 | |
| Pro | Arg | Trp | Phe | Asp | Leu | Thr | Asp | Glu | Val | Thr | Pro | Thr | Pro | Trp | Gly | | |
| | | | | 300 | | | | | 305 | | | | | 310 | | | |
| gac | ttg | gaa | gtt | tac | caa | tac | aac | ggt | aaa | tat | acc | caa | cat | tgt | gct | 1012 | |
| Asp | Leu | Glu | Val | Tyr | Gln | Tyr | Asn | Gly | Lys | Tyr | Thr | Gln | His | Cys | Ala | | |
| | | | 315 | | | | | 320 | | | | | 325 | | | | |
| gcc | gtt | gat | agt | tct | gag | tgc | att | gaa | gtg | cct | gac | atc | aga | cca | gaa | 1060 | |
| Ala | Val | Asp | Ser | Ser | Glu | Cys | Ile | Glu | Val | Pro | Asp | Ile | Arg | Pro | Glu | | |
| | | 330 | | | | | 335 | | | | | 340 | | | | | |
| ttc | aac | cct | tgg | caa | tat | gat | aat | ttg | gat | gct | gaa | tag | tgagcatcct | | | 1109 | |
| Phe | Asn | Pro | Trp | Gln | Tyr | Asp | Asn | Leu | Asp | Ala | Glu | | | | | | |
| | 345 | | | | | 350 | | | | | 355 | | | | | | |
| tgtggaattc | tttctatttt | tttgaaatat | cattttgtta | ttaagtttgt | aatgtaatct | | | | | | | | | | | 1169 | |
| tgattggaat | gcttgaaatt | tggttttgtt | tttgggttgt | tttatcactg | tagtatttga | | | | | | | | | | | 1229 | |
| ttaattaata | gtagctatgt | tagttcatca | gttcactttg | catggataaa | tgctagtaga | | | | | | | | | | | 1289 | |
| gaaattaaag | ttaaaaaaaa | aaaaaaaaaa | aaaaaaaaaa | aaaaaaaaaa | aaaagggcgg | | | | | | | | | | | 1349 | |
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| tca tgg agt agc ttc ctg aag tcc atc gca tcc ttc aac ggc gac ctc | 96 |
| Ser Trp Ser Ser Phe Leu Lys Ser Ile Ala Ser Phe Asn Gly Asp Leu | |
| 20 25 30 | |
| tcc tct ctc acc gca ccg ccg ttc atc ctc tca aca acc tct tta acc | 144 |
| Ser Ser Leu Thr Ala Pro Pro Phe Ile Leu Ser Thr Thr Ser Leu Thr | |
| 35 40 45 | |
| gag tat tct gcg tac tgg tgc gaa cat cct gca ctc ttc gtt gcc ccc | 192 |
| Glu Tyr Ser Ala Tyr Trp Cys Glu His Pro Ala Leu Phe Val Ala Pro | |
| 50 55 60 | |
| gca cgt gag ccc gat cct gcg aag aga gcg ctc ttg gtg ctg aaa tgg | 240 |
| Ala Arg Glu Pro Asp Pro Ala Lys Arg Ala Leu Leu Val Leu Lys Trp | |
| 65 70 75 80 | |
| ttc ctg agc aca ttg cac caa cag tac tgc tct cga agc gaa aag cta | 288 |
| Phe Leu Ser Thr Leu His Gln Gln Tyr Cys Ser Arg Ser Glu Lys Leu | |
| 85 90 95 | |
| gga agc gag aaa aag ccg ctc aac ccg ttc ctg ggc gag ctt ttc ctg | 336 |
| Gly Ser Glu Lys Lys Pro Leu Asn Pro Phe Leu Gly Glu Leu Phe Leu | |
| 100 105 110 | |
| ggc aag tgg ata gag gat gag gat gtg ggc gag aca agg ttg atc agc | 384 |
| Gly Lys Trp Ile Glu Asp Glu Asp Val Gly Glu Thr Arg Leu Ile Ser | |
| 115 120 125 | |
| gag caa gtc agc cat cat cct cct gcg aca gcg tat tca ata gtc aat | 432 |
| Glu Gln Val Ser His His Pro Pro Ala Thr Ala Tyr Ser Ile Val Asn | |
| 130 135 140 | |
| gag aaa cat gga gtt gag ctc caa gga tac aac gcc caa aaa gcc tcc | 480 |
| Glu Lys His Gly Val Glu Leu Gln Gly Tyr Asn Ala Gln Lys Ala Ser | |
| 145 150 155 160 | |
| ttc tcc agc acc atc caa gtg aaa caa cta ggc cac gcc tat ctc tcc | 528 |
| Phe Ser Ser Thr Ile Gln Val Lys Gln Leu Gly His Ala Tyr Leu Ser | |
| 165 170 175 | |
| tta acg ccg ccc gga aaa gat gca aac aac gaa gac gac cgt gag cac | 576 |
| Leu Thr Pro Pro Gly Lys Asp Ala Asn Asn Glu Asp Asp Arg Glu His | |
| 180 185 190 | |
| tac ctc atc acc ctc ccc aac ctc cac atc gaa tcc ctg atc tat ggg | 624 |

| | | | | | | | | | | | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Tyr | Leu | Ile | Thr | Leu | Pro | Asn | Leu | His | Ile | Glu | Ser | Leu | Ile | Tyr | Gly | |
| | 195 | | | | | | 200 | | | | | 205 | | | | |
| aca | cca | ttc | gtt | gaa | ttg | gaa | aag | agt | tgc | aag | atc | gcc | agc | tca | acc | 672 |
| Thr | Pro | Phe | Val | Glu | Leu | Glu | Lys | Ser | Cys | Lys | Ile | Ala | Ser | Ser | Thr | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| ggg | tac | atc | tct | aag | ata | gac | ttt | tcg | ggc | aaa | ggc | tgg | ctg | agc | gga | 720 |
| Gly | Tyr | Ile | Ser | Lys | Ile | Asp | Phe | Ser | Gly | Lys | Gly | Trp | Leu | Ser | Gly | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| aag | aaa | aat | acc | ttc | tcc | gca | gtg | tta | tac | aag | gaa | agc | gac | ggc | gaa | 768 |
| Lys | Lys | Asn | Thr | Phe | Ser | Ala | Val | Leu | Tyr | Lys | Glu | Ser | Asp | Gly | Glu | |
| | | | 245 | | | | | | 250 | | | | | 255 | | |
| aaa | aat | cct | tta | tac | aca | gcc | gac | ggg | caa | tgg | tcg | agc | agc | ttc | act | 816 |
| Lys | Asn | Pro | Leu | Tyr | Thr | Ala | Asp | Gly | Gln | Trp | Ser | Ser | Ser | Phe | Thr | |
| | | 260 | | | | | | 265 | | | | | 270 | | | |
| atc | cgc | gat | gca | cgc | gct | aag | aag | gat | att | gag | acc | ttc | act | atc | agc | 864 |
| Ile | Arg | Asp | Ala | Arg | Ala | Lys | Lys | Asp | Ile | Glu | Thr | Phe | Thr | Ile | Ser | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| aat | ctg | aaa | aca | acc | ccc | tta | aca | gtc | gcc | cct | ctt | gat | gaa | caa | gat | 912 |
| Asn | Leu | Lys | Thr | Thr | Pro | Leu | Thr | Val | Ala | Pro | Leu | Asp | Glu | Gln | Asp | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| gaa | tgg | gaa | act | cgc | cgt | gca | tgg | cgc | gac | gta | gca | gcc | gcc | atc | gaa | 960 |
| Glu | Trp | Glu | Thr | Arg | Arg | Ala | Trp | Arg | Asp | Val | Ala | Ala | Ala | Ile | Glu | |
| | 305 | | | | 310 | | | | | 315 | | | | | 320 | |
| cgc | ggc | gac | atg | gaa | gcc | aca | tca | aac | gcc | aaa | acc | aag | atc | gaa | gtc | 1008 |
| Arg | Gly | Asp | Met | Glu | Ala | Thr | Ser | Asn | Ala | Lys | Thr | Lys | Ile | Glu | Val | |
| | | | 325 | | | | | | 330 | | | | | 335 | | |
| gcg | caa | cga | gaa | ctc | cgc | aaa | aag | gag | aaa | gag | caa | ggc | gag | gag | tgg | 1056 |
| Ala | Gln | Arg | Glu | Leu | Arg | Lys | Lys | Glu | Lys | Glu | Gln | Gly | Glu | Glu | Trp | |
| | | 340 | | | | | | 345 | | | | 350 | | | | |
| gaa | cga | cga | ttc | ttc | aag | cga | gtc | aac | gaa | aag | gat | gaa | cct | acc | ttt | 1104 |
| Glu | Arg | Arg | Phe | Phe | Lys | Arg | Val | Asn | Glu | Lys | Asp | Glu | Pro | Thr | Phe | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| atg | aga | ttg | gcg | gcg | atg | ctg | gat | ttg | acg | caa | ggc | atc | gaa | agt | gac | 1152 |
| Met | Arg | Leu | Ala | Ala | Met | Leu | Asp | Leu | Thr | Gln | Gly | Ile | Glu | Ser | Asp | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| cgc | acc | ggg | gga | gtt | tgg | agg | ttt | gat | cct | tca | cgt | gct | gtg | gat | gcg | 1200 |
| Arg | Thr | Gly | Gly | Val | Trp | Arg | Phe | Asp | Pro | Ser | Arg | Ala | Val | Asp | Ala | |
| | 385 | | | | 390 | | | | | 395 | | | | | 400 | |
| aat | ccg | ccg | tat | cac | aag | gtt | ggc | ggc | gaa | ggg | ttg | gga | ttg | taa | | 1245 |
| Asn | Pro | Pro | Tyr | His | Lys | Val | Gly | Gly | Glu | Gly | Leu | Gly | Leu | | | |
| | | | 405 | | | | | 410 | | | | | | | | |
| tttatttatg | aggcatcttt | tatatattcat | aaaaacaggg | tctaggccgt | ttattcatta | | | | | | | | | | | 1305 |

aatgtgtatt aagtagcgct ttttctcgac cggttgagatt catggatgca agtgtaccta 1365
 atagctcaat gcgagactct ttccaagcaa aaaaaaaaaa aaaaaaaggg cggccgc 1422

<210> 5
 <211> 2126
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>
 <221> CDS
 <222> (453)...(1757)

<400> 5

aacctctccg cccgtatatt ttttttaata tgttaaatag tgatagaact gataagcctc 60
 atttttctttt attgggctcc aagacgcgaa ctgttcgtag ggtaaccggt tgacaccta 120
 acgacctttc agcctcacct gcagtatttc ttcaacaacg cctgtcgcta tgttaaataa 180
 tagcaatcgt ttgtgatcac cattgtcgaa tttgacgcgc ttaaacaaaa accattgttt 240
 tggcctcggt ccctgcattc aacaaaagag caaggatatgc cgtcaaacag tcgttaaaag 300
 agaaggttta taaactatct tgttttgtac tttgctgtcc cggatccagt tgggtcttct 360
 tttcaacctg tctgagtcg atctttcttt ccctacttga agctccatat atctaagtca 420
 tctaagtgtat tctgtctaga ttacaaacga aa atg tct caa cac gca agc tca 473
 Met Ser Gln His Ala Ser Ser
 1 5
 tct tct tgg act tct ttt ttg aaa tcg ata agt tcg ttc aac gga gat 521
 Ser Ser Trp Thr Ser Phe Leu Lys Ser Ile Ser Ser Phe Asn Gly Asp
 10 15 20
 cta tcg tct ttg tct gca cca ccg ttt att ctt tct ccc act tcc tta 569
 Leu Ser Ser Leu Ser Ala Pro Pro Phe Ile Leu Ser Pro Thr Ser Leu
 25 30 35
 aca gag ttt tct cag tat tgg gct gaa cat cca gct tta ttt ctg gag 617
 Thr Glu Phe Ser Gln Tyr Trp Ala Glu His Pro Ala Leu Phe Leu Glu
 40 45 50 55
 cct tcg ttg att gat ggt gaa aac tac aaa gat cac tgt ccc ttt gac 665
 Pro Ser Leu Ile Asp Gly Glu Asn Tyr Lys Asp His Cys Pro Phe Asp
 60 65 70
 cca aat gtg gaa tca aag gaa gtg gcg cag atg ttg gcg gtt gtt agg 713
 Pro Asn Val Glu Ser Lys Glu Val Ala Gln Met Leu Ala Val Val Arg
 75 80 85
 tgg ttt att tct act ttg aga tct caa tac tgc tct aga agc gaa tcg 761
 Trp Phe Ile Ser Thr Leu Arg Ser Gln Tyr Cys Ser Arg Ser Glu Ser
 90 95 100

| | |
|---|------|
| atg ggt tct gaa aag aag cct ttg aac cca ttc ttg ggt gag gta ttt | 809 |
| Met Gly Ser Glu Lys Lys Pro Leu Asn Pro Phe Leu Gly Glu Val Phe | |
| 105 110 115 | |
| ggt gga aag tgg aaa aat gat gag cat cca gag ttt ggt gaa acg gtt | 857 |
| Val Gly Lys Trp Lys Asn Asp Glu His Pro Glu Phe Gly Glu Thr Val | |
| 120 125 130 135 | |
| ctt tta agt gag caa gtt tca cat cat cca cct atg aca gca ttt tcg | 905 |
| Leu Leu Ser Glu Gln Val Ser His His Pro Pro Met Thr Ala Phe Ser | |
| 140 145 150 | |
| att ttt aat gaa aaa aat gat gtt tct gtt caa gga tac aat caa att | 953 |
| Ile Phe Asn Glu Lys Asn Asp Val Ser Val Gln Gly Tyr Asn Gln Ile | |
| 155 160 165 | |
| aaa act ggt ttt acc aaa aca ttg acg cta acg gtc aaa cca tac ggg | 1001 |
| Lys Thr Gly Phe Thr Lys Thr Leu Thr Leu Thr Val Lys Pro Tyr Gly | |
| 170 175 180 | |
| cat gtc att ttg aag att aaa gat gag acc tac ctg att aca acc ccg | 1049 |
| His Val Ile Leu Lys Ile Lys Asp Glu Thr Tyr Leu Ile Thr Thr Pro | |
| 185 190 195 | |
| cct ttg cat atc gaa ggt att tta gtc gct tct cca ttt gtt gaa tta | 1097 |
| Pro Leu His Ile Glu Gly Ile Leu Val Ala Ser Pro Phe Val Glu Leu | |
| 200 205 210 215 | |
| gga ggc agg tca ttc ata cag tca tca aat ggt atg tta tgt gtt ata | 1145 |
| Gly Gly Arg Ser Phe Ile Gln Ser Ser Asn Gly Met Leu Cys Val Ile | |
| 220 225 230 | |
| gaa ttt tca gga agg ggg tat ttc aca ggg aag aag aac tcc ttt aag | 1193 |
| Glu Phe Ser Gly Arg Gly Tyr Phe Thr Gly Lys Lys Asn Ser Phe Lys | |
| 235 240 245 | |
| gca aga att tac aga agc cca caa gag cat agt cat aaa gaa aat gcg | 1241 |
| Ala Arg Ile Tyr Arg Ser Pro Gln Glu His Ser His Lys Glu Asn Ala | |
| 250 255 260 | |
| cta tac cta atc tct ggc caa tgg tca ggt gtt tca aca att ata aaa | 1289 |
| Leu Tyr Leu Ile Ser Gly Gln Trp Ser Gly Val Ser Thr Ile Ile Lys | |
| 265 270 275 | |
| aaa gac tcg caa gtt tca cat cag ttt tac gat tca tcg gaa act cct | 1337 |
| Lys Asp Ser Gln Val Ser His Gln Phe Tyr Asp Ser Ser Glu Thr Pro | |
| 280 285 290 295 | |
| act gaa cat tta tta gtt aag cca atc gaa gaa caa cat cct ctg gaa | 1385 |
| Thr Glu His Leu Leu Val Lys Pro Ile Glu Glu Gln His Pro Leu Glu | |
| 300 305 310 | |
| agt agg agg gca tgg aag gat gtg gca gaa gca atc aga caa gga aat | 1433 |
| Ser Arg Arg Ala Trp Lys Asp Val Ala Glu Ala Ile Arg Gln Gly Asn | |
| 315 320 325 | |

| | |
|---|------|
| att agt atg ata aaa aag act aag gaa gaa cta gaa aat aag caa aga | 1481 |
| Ile Ser Met Ile Lys Lys Thr Lys Glu Glu Leu Glu Asn Lys Gln Arg | |
| 330 335 340 | |
| gcc ttg aga gaa caa gaa cgc gta aaa ggt gtg gaa tgg caa aga aga | 1529 |
| Ala Leu Arg Glu Gln Glu Arg Val Lys Gly Val Glu Trp Gln Arg Arg | |
| 345 350 355 | |
| tgg ttc aaa caa gtg gac tac atg aat gaa aat aca tca aat gat gta | 1577 |
| Trp Phe Lys Gln Val Asp Tyr Met Asn Glu Asn Thr Ser Asn Asp Val | |
| 360 365 370 375 | |
| gag aaa gca agt gaa gat gat gcc ttt agg aaa ttg gcg tcc aaa ctg | 1625 |
| Glu Lys Ala Ser Glu Asp Asp Ala Phe Arg Lys Leu Ala Ser Lys Leu | |
| 380 385 390 | |
| cag ctt tct gtg aaa aat gtg cca agt ggg aca ttg att ggc ggc aaa | 1673 |
| Gln Leu Ser Val Lys Asn Val Pro Ser Gly Thr Leu Ile Gly Gly Lys | |
| 395 400 405 | |
| gat gat aag aaa gat gtt tca acc gca ttg cat tgg agg ttt gat aaa | 1721 |
| Asp Asp Lys Lys Asp Val Ser Thr Ala Leu His Trp Arg Phe Asp Lys | |
| 410 415 420 | |
| aat ttg tgg atg agg gag aac gaa att act ata taa tataaatgtt | 1767 |
| Asn Leu Trp Met Arg Glu Asn Glu Ile Thr Ile | |
| 425 430 | |
| ttttaaagaa taaatatcaa aaattaatac taattgatgt ttgcattgct ttttttaagg | 1827 |
| gaaaatgcaa gcgtttttat ttttaacttt tggttttgaa gctcgtaatt caacaaaaaa | 1887 |
| gaattaaata atcttcaagt ccgataacaa gatgtagaaa aaacatccca atgaagttac | 1947 |
| aagtcaaacc attcactgag aatttttgta actcaccacc gatttttttg ataaaatgta | 2007 |
| ttcctgcaac tttttttttt gaagagataa aaagaattga atagaatatg cagtaaaaaa | 2067 |
| agaatctcga aaaaaaaagg acaagaaatc ttaactacca tcaaacaatt gaaaattga | 2126 |
| <210> 6 | |
| <211> 266 | |
| <212> DNA | |
| <213> Glycine max | |
| <400> 6 | |
| ccattcaatc caattcttgg tgagacttat gaaatgggta accatggtgg cattacattt | 60 |
| atatcagagc aggtcagtca tcaccctcca atgagtgctg ggcatgctga aactgaacat | 120 |
| ttcacttatg atgttacatc aaaattgaaa accaaatttc tcggcaactc agttgatgta | 180 |
| tatcctgttg gaagaacgcg tgttaccctc aaaagagatg gtgtgggcct tgatttggtg | 240 |
| cctcctccta caaaagttag caactt | 266 |

<210> 7
 <211> 291
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (1)...(291)
 <223> Unsure at all n locations

<400> 7

tcacaacttc agtgctatgg tgaatcagtg tattgcacag gttcggactt gctaagcatg 60
 tgcaacaatg gtcagagtcc acttgatagg ttcatatctg tggtagcatg gtgcatatct 120
 accactcgcc ctgtgacttt tgggtgttgct ccttataatc ccantottgg tgagacacac 180
 cncgtttcaa ggggaaatct taatgtgtta ttggagcaga tttcacatca ccctccagta 240
 actgctctcc atgcaacaga tgaganggaa aacattgaaa tgttatggtg c 291

<210> 8
 <211> 282
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (1) ... (282)
 <223> Unsure at all n locations

<400> 8

gtgccagng acaggtctgg tagctgaaat atcatacatg atcaagccat tgctttttta 60
 ggatttnggg gaagtcgtaa attgatcaaa gggnaaatcc ttgactcatn attactcaaa 120
 ggtctctgcg aagttgatng tcattgggat aagatagtta gagtgaagga tacnaatagt 180
 gnagaagtga gagtgatata tgatgccaaa gaagcctttt caggtctcaa aactcctatt 240
 atcaaggatg tggagagtgt gtggccaacc gaatcagccc tt 282

<210> 9
 <211> 255
 <212> DNA
 <213> Glycine max

<400> 9

gtaactccta ccccttgggg tgacttgga gtttaccat acaacggtaa atatacccaa 60

cattgtgctg ccgttgatag ttctgagtgc attgaagtgc ctgacatcag accagaattc 120
aacccttggc aatatgataa ttggatgct gaatagtga catccttgtg gaattctttc 180
tatttttttt aaatatcatt ttgttattaa gtttgtaatg taatcttgat tggaagcttg 240
aaatttggtt ttgtt 255

<210> 10
<211> 250
<212> DNA
<213> Glycine max

<400> 10

taactcctac cccttggggt gacttgggaag ttaccaata caacggtaaa tatacccaac 60
attgtgctgc cggttgatag tctgagtgc ttgaagtgcc tgacatcaga ccagaattca 120
acccttggca atatgataat ttggatgctg aatagtgagc atccttgttg aattctttct 180
atttttttta aatatcattt tgttattaag tttgtaatgt aatcttgatt ggaatgcttg 240
aaatttggtt 250

<210> 11
<211> 283
<212> DNA
<213> Glycine max
<220>
<221> unsure
<222> (1) ... (283)
<223> Unsure at all n locations

<400> 11

cgctgtgnt taatttccca aaatctcaac ttcaatgcta nggtgaatca gtgtactgca 60
catcttccaa cttgctaagc caatgcaaac agtgggcaga gtccactgga caggttcaca 120
tcagtagtag catggagcat atctaccaca cgccccacat cttttggtgt tgctccttat 180
aattccactc ttggagagac ccacatggt tccaaggga atctcaacgt cctagttgag 240
caggtttcac tcaatctctc agtatctgcc ctccatgcaa cag 283

<210> 12
<211> 255
<212> DNA
<213> Glycine max

<400> 12

ggagagtgtg tggccaaccg aatcagccct tgtttgaggt gagttgagcc aagccattat 60
gaacaaagat tgggaaagag caagagaagc aaagcaagac gtggaagaaa gacagaggaa 120
tatgttgaga gacagagcca tgaaaggaga aacttggttt cctaagaatt ttaggggtgc 180
ttacagtaaa gacacatggg aatgggactg ttcaccaact cataaatggg tccctgaggc 240
cccatcata gctca 255

<210> 13
<211> 259
<212> DNA
<213> Glycine max
<220>
<221> unsure
<222> (1) ... (259)
<223> Unsure at all n locations

<400> 13
agtcaaccct ccagtatctg ccctccatgc aacagatgag anggaaaaca ttgagatgat 60
atggtcccag caacctgttc caaagtttcg ggggtacatct atgaagctca agtgcattgg 120
aaacgtcata tgtttctcca tgatttagga gtttcagctg acgtttacca tgcacttgag 180
ctgangctcc taaatcatgg agaaacatat gaaatgaatt gtcttcacct ttcaattaga 240
attcttccgg ttctggga 259

<210> 14
<211> 355
<212> DNA
<213> Glycine max
<220>
<221> unsure
<222> (1) ... (355)
<223> Unsure at all n locations

<400> 14
gcagcttttg ctgtgtctag ctatgcgtca actgaangtc gacaatgtaa accttttaat 60
cctttactcg gggagacctc cgaagctgac tatccagata aaggacttaa gtttttttct 120
gaaaagggtta gtcatcatcc aatgattgtt gcttgtcact gtgagggaag gggatggaag 180
ttttgggcag attctaattt gaaaggaaaa ttctgggggc gttctatcca gttagatcct 240
gtgggtgtcc tcaactctaca gtttgaggat ggtgaaacat ttcagtggag caaggtcacc 300

ccatggcagt atggtaattt ggccacggaa tgaactagtt tcaatttctt tggttttgga 180
 tgntncagtt agttcatgta actntttnncn antganacna gaanacaact ncctncnnca 240
 ncnnanngtt agttgggcng tgtacgc 267

<210> 18
 <211> 252
 <212> DNA
 <213> Glycine max

<400> 18

gtcttataga gctcccaatc tctacatcg cttgttaagt ttactcaaga acgtgcggcc 60
 aggatcagat ctacacact tccaactgcc agctgtgttt aacttcccaa aatctcaact 120
 tcaatgctat ggtgaatcag tgtactgcac atcttcaaac ttgctgagca aatgcaacaa 180
 tgggcagagt ccactggaca ggttcacatc agtagtagca tggagcatat ctaccacacg 240
 cccacatct tt 252

<210> 19
 <211> 241
 <212> DNA
 <213> Glycine max

<400> 19

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 gttacatcaa aattgaaaac caaatttctc ggcaactcag ttgatgtata tcctgttgga 120
 agaacgcgtg ttaccctcaa aagagatggt gtggctccttg atttggtgcc tcctcctaca 180
 aaagttagca acttgatattt tggacgaact tggattgatt caccaggaga gatgatcctg 240
 a 241

<210> 20
 <211> 262
 <212> DNA
 <213> Glycine max

<400> 20

tctcgagcct attcggtcg aggccaaaga agccatttca ggtcactaaa ctctattat 60
 catatgatgt ggagagtgtg tattcaaccg aatcagccct tgtttggagt gagttgagcc 120
 aagccattat gaacaaagat tgggaaagag caagagaagc aaagcaagac gtggaagaaa 180

gacagaggaa tatgttgaga gacagagcca tgacaggaga aactggttgt ctaagaattt 240
agggtgtctt acagtaaaga ca 262

<210> 21
<211> 463
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> unsure
<222> (1) ... (463)
<223> Unsure at all n locations

<400> 21

ggggaacccc ttccaggaa agagctgaaa gaggtgtggc atttggctga tgtcccaaaa 60
aacgacaact ttcagtacac tcactttgct cacaagataa acagcttcga cacagcgcct 120
gctaagctct tggcttcaga ctacgtatc cgtcctgata gatattccct tgagcagggg 180
gacctttcta aagctggttc cgagaaacac agccttgagg agagacaaaag ggccgaaaag 240
aggaccagag agacaaaagg acaaaagtgc actccaagat ggttcgatct aacggatgag 300
atcacaccta ctccatgggg agatattgaa gtataccant acaacgggaa gtacaatgaa 360
caccgagaca cggcagagag ctcaagtagt gcctccaacg aaacgggact caaatccatc 420
gagtttaatc cttggcaata tggtaatatc tcaaccgaat gaa 463

<210> 22
<211> 399
<212> DNA
<213> Arabidopsis thaliana

<400> 22

agtgaacctc tcccaggcac cgaactgaaa gaggtatgga aactcgctga tgtgccaaaag 60
gatgacaaat atcaatacac tcactttgct cacaagatta atagcttcga cactgccccg 120
aaaaagctgt tgccctctga ttcacgggta cgacctgata gatacgact tgagatgggc 180
gacatgtcca aatcaggcta tgagaagagc agcatggaag agagacagag agctgacaag 240
agaacccgcg aacataaagg ccaagccttt actccaaaat ggttcgatgt aacggaagaa 300
gtcactgcta caccatgggg tgatctggaa gtttaaccaat tcaactggaaa gtactcagaa 360
catcgtgcag ctgcggataa ctctgaagat aagaccgac 399

<210> 23

<211> 343
 <212> DNA
 <213> Arabidopsis thaliana

<400> 23

acggacgcgt gggcaactcc aatgttacgg cgagatggtc tacagcttcg tcggtcagga 60
 tctgcttggg gaatgcagcc gccgtgatct tcccattgaa cggctcaaata cagtggtagc 120
 gtggaacatc tccacactcc gtccgggtggc ctttggcatg tctccgtaca actccgttct 180
 cggcgagact caccacgtat cgaacgggtc catcaacgtc atcgccgaac aagtagtgca 240
 tcatcctccg gtttccgctc ttcattgcgc tcacgaacaa gaaaatatcg acgtgacatg 300
 gtgtcaatat ttcactccta aatttcgtgg tactcacgtg gac 343

<210> 24
 <211> 510
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> unsure
 <222> (1) ... (510)
 <223> Unsure at all n locations

<400> 24

gaaagctagc agatgtagaa caaagttttt tgtaactacg agagaataag aatacatttg 60
 tttccaaaaa gatttgatct tttctgtctt ttggagcgat acatttaagt agacagatct 120
 tggaattgcc atgggttgaa ttggatcgac ttagggtcgg tggtatcttc agagttatcc 180
 gcagctgcac gatgttccga gtactttcca ttgaattggc aaacttccag atcaccat 240
 ggtgtagcag tgacttcttc cgttacatcg aaccattttg gagtaaaggc ttggcctttc 300
 tcttcgctgg gtcncttttc aagtctctgt cncctttcca tgggtgntctt cccanagcct 360
 gatttgnaca tggcgccan cccaaggng gatcaatcag gccgnaacgg ggaatcaggn 420
 ggnaacagct tttcnggna ntgncgaagc aataaacnt gggggcaaag gggggggatt 480
 ggaaattggc aacccttggc naacaggggc 510

<210> 25
 <211> 282
 <212> DNA
 <213> Arabidopsis thaliana

<220>

<221> unsure
<222> (1) ... (282)
<223> Unsure at all n locations

<400> 25

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agagaagaga aaggccaaaa ntttcncca aaatggtttn atgaaacana agangtcact 120
cctacaccat ggggtgatct cgaagtttac caattcantg gaaagtactc ggtgcaccgn 180
gccacagctg aaaactntga ggatacaacc gntgtgaagt tgncccaatt caacccttgg 240
caattccaag atctctntgc ttaatccttt ggtgccattt gt 282

<210> 26
<211> 380
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> unsure
<222> (1) ... (380)
<223> Unsure at all n locations

<400> 26

cgttggtggc ngcggaagtg gtttcttcgc ctctcttgct tcgtcgatct ccaatttngg 60
ntctgctatg accaaatcag ttaatggttt ggttccttat gagggacttg aagttatcaa 120
tcctgaagga agtacagatg atgctgagga ggaagcaagc agaggaagat ggaagcaaga 180
ggatcgagat ggctattgga agatgatgca gaagtacata ggatctgatg ttacatcaat 240
ggtgaccctt cctgtgatta tttttgaacc aatgacaatg cttcagaaaa tggcggagtt 300
gatggaatac tcgcatctgc tagacatggc agacaaaacc gaggaccctt atttncgcat 360
ggtgtatgca tcatcgtggg 380

<210> 27
<211> 359
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> unsure
<222> (1) ... (359)
<223> Unsure at all n locations

<400> 27

ggtaatgaag gagttgaggt cataaatcca gaaggtggca aggaagatnc tgaagaggaa 60

gctcagaaaag gaaggtggaa ggacgaggaa cgagatagtt actggaagat gatgcagaaa 120
 tatataggtt cggatattac gtcaatggtg gctcttctg ttgtnatatt tnanctatg 180
 actatnctcc anaagatggc tgagataatg gagtattctc atttnttga tcaagcagat 240
 gaatgcngag atccatactt gctgttagta tatccttcat catgggggtat atctgtttac 300
 tatggccttc caacggacct tggaagcctt tnaatccnat tcttgggggg gnnanttna 359

<210> 28
 <211> 510
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> unsure
 <222> (1) ... (510)
 <223> Unsure at all n locations

<400> 28
 aaaagagaaa agtgttagcc tttggtcaat gatcaaagac antataggga aggntctcac 60
 aaaagtctgt cttctgtttt acttcaacga gccactttct tctttacaga aatgttttga 120
 ggatttgga tattcgtacc ttcttgaccg agcatttgaa tatggcaaaa ggggaaatag 180
 cctcatgagg atacttaatg tagctgcttt tgctgtatct gggtatgcat caactgaagg 240
 aagaatttgc aaacctttta atccattggt aggtgaaaca tacngggcag actatccaga 300
 caaaggcctt cggttttttt ccaggaaagg tcagtcatca tcctatgggt gtcgnatgcc 360
 attgtgatgg caccnggtgg gaattcttgg gggacagcaa tcttnggggc aaattttggg 420
 gcgntctntt tagcttnacc cccttgggga ttinncttna aattnatgat ggggaanccn 480
 caggggggaa ggngcccacc atnncaaacc 510

<210> 29
 <211> 493
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> unsure
 <222> (1) ... (493)
 <223> Unsure at all n locations

<400> 29
 cccnccng aaagnttccc ctgtttccgg nttnnccnt ntgnccccc ttgggggggn 60

cctttcccaa tnggnnttgg gngngccccc ttggangggg ccggggcttt aaagggcccc 120
 ncgnagggaa ggccagcctt tctcccaaatt ggtcgaatga ccggaggaag tctactgtac 180
 cccatgggggt gatctggaag tttcccaatt caatggaaaag tactcggaac atcgtgcagc 240
 tgcggataac tctgaagata acaccgaccc taagtcgac caattcaacc catggcaatt 300
 ccaagatctg tctacttaaa tgtatcgctc caaaagacag aaaagatcaa atcttttttg 360
 aaacaaatgt attcttattc tctcgtagtt acaaaaaact ttgttctaca tctgctagct 420
 ttcccatgtc tttctctagt attagtgtac aacttctact gttttgtctt aaattcattc 480
 aaatctttct ttg 493

<210> 30
 <211> 358
 <212> PRT
 <213> Glycine max

<400> 30

Met Thr Met Leu Gln Lys Met Ala Glu Leu Met Glu Tyr Ser Tyr Leu
 1 5 10 15
 Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Met Arg Leu Val Tyr
 20 25 30
 Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr Ala Tyr Gln Arg Thr Trp
 35 40 45
 Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu Met Val Asn His
 50 55 60
 Gly Gly Ile Thr Phe Ile Ser Glu Gln Val Ser His His Pro Pro Met
 65 70 75 80
 Ser Ala Gly His Ala Glu Thr Glu His Phe Thr Tyr Asp Val Thr Ser
 85 90 95
 Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Val Asp Val Tyr Pro Val
 100 105 110
 Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val Val Leu Asp Leu
 115 120 125
 Val Pro Pro Pro Thr Lys Val Ser Asn Leu Ile Phe Gly Arg Thr Trp
 130 135 140
 Ile Asp Ser Pro Gly Glu Met Ile Leu Thr Asn Leu Thr Thr Gly Asp
 145 150 155 160
 Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe Gly Tyr Glu Val
 165 170 175

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Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu Pro Lys Ile Leu Met Thr
180 185 190

Gly Lys Trp Asn Glu Ala Met Asn Tyr Gln Val Cys Asp Ser Glu Gly
195 200 205

Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu Ile Trp Arg Val Ala Asp
210 215 220

Thr Pro Lys Lys Asp Lys Phe Gln Tyr Thr His Phe Ala His Lys Ile
225 230 235 240

Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu Leu Ala Ser Asp Ser Arg
245 250 255

Leu Arg Pro Asp Arg Met Ala Leu Glu Lys Gly Asp Leu Ser Thr Ser
260 265 270

Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg Gln Arg Ala Glu Lys Arg
275 280 285

Asn Arg Glu Ala Lys Gly His Lys Phe Thr Pro Arg Trp Phe Asp Leu
290 295 300

Thr Asp Glu Val Thr Pro Thr Pro Trp Gly Asp Leu Glu Val Tyr Gln
305 310 315 320

Tyr Asn Gly Lys Tyr Thr Gln His Cys Ala Ala Val Asp Ser Ser Glu
325 330 335

Cys Ile Glu Val Pro Asp Ile Arg Pro Glu Phe Asn Pro Trp Gln Tyr
340 345 350

Asp Asn Leu Asp Ala Glu
355

<210> 31
<211> 300
<212> PRT
<213> Glycine max

<400> 31

Met Cys Asn Asn Gly Gln Ser Pro Leu Asp Arg Phe Ile Ser Val Val
1 5 10 15

Ala Trp Cys Ile Ser Thr Thr Arg Pro Val Thr Phe Gly Val Ala Pro
20 25 30

Tyr Asn Pro Ile Leu Gly Glu Thr His His Val Ser Arg Gly Asn Leu
35 40 45

Asn Val Leu Leu Glu Gln Ile Ser His His Pro Pro Val Thr Ala Leu
50 55 60

His Ala Thr Asp Glu Lys Glu Asn Ile Glu Met Leu Trp Cys Gln Arg

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| | | | | | | |
|---|-----|----|--|-----|--|-----|
| 65 | | 70 | | 75 | | 80 |
| Pro Asp Pro Lys Phe Asn Gly Thr Ser Val Glu Ala Lys Val His Gly | | | | | | |
| | 85 | | | 90 | | 95 |
| Ile Arg Gln Leu Lys Leu Leu Asn His Gly Glu Thr Tyr Glu Met Asn | | | | | | |
| | 100 | | | 105 | | 110 |
| Cys Pro Arg Leu Leu Leu Arg Ile Leu Pro Val Pro Gly Ala Asp Trp | | | | | | |
| | 115 | | | 120 | | 125 |
| Ala Gly Thr Val Asn Ile Arg Cys Leu Glu Thr Gly Leu Val Ala Glu | | | | | | |
| | 130 | | | 135 | | 140 |
| Leu Ser Tyr Arg Ser Ser Ser Phe Leu Gly Ile Gly Gly Asn His Arg | | | | | | |
| | 145 | | | 150 | | 155 |
| Val Ile Lys Gly Lys Ile Leu Asp Ser Ser Ser Leu Lys Val Leu Tyr | | | | | | |
| | 165 | | | 170 | | 175 |
| Glu Val Asp Gly His Trp Asp Arg Thr Val Lys Val Lys Asp Thr Asn | | | | | | |
| | 180 | | | 185 | | 190 |
| Asn Gly Lys Val Arg Val Ile Tyr Asp Ala Lys Glu Val Met Ser Gly | | | | | | |
| | 195 | | | 200 | | 205 |
| Leu Glu Thr Pro Ile Leu Lys Asp Ile Glu Gly Val Trp Gln Thr Glu | | | | | | |
| | 210 | | | 215 | | 220 |
| Ser Ala His Val Trp Gly Glu Leu Asn Gln Ala Ile Val Ser Lys Asp | | | | | | |
| | 225 | | | 230 | | 235 |
| Trp Glu Lys Ala Arg Glu Ala Lys Leu Lys Val Glu Glu Arg Gln Arg | | | | | | |
| | 245 | | | 250 | | 255 |
| Glu Leu Val Arg Glu Arg Glu Ser Lys Gly Glu Thr Trp Ile Ser Lys | | | | | | |
| | 260 | | | 265 | | 270 |
| His Phe Val Val Ser Asn Asn Lys Glu Gly Trp Gln Cys Ser Pro Ile | | | | | | |
| | 275 | | | 280 | | 285 |
| His Lys Ser Val Pro Ala Ala Pro Ile Thr Ala Leu | | | | | | |
| | 290 | | | 295 | | 300 |

<210> 32
 <211> 355
 <212> PRT
 <213> Glycine max

<400> 32

| | | | | | | |
|---|----|---|--|----|----|----|
| Met Ala Glu Leu Met Glu Tyr Ser Tyr Leu Leu Asp Met Ala Asp Lys | | | | | | |
| 1 | | 5 | | | 10 | 15 |
| Thr Glu Asp Pro Tyr Met Arg Leu Val Tyr Ala Ser Ser Phe Phe Ile | | | | | | |
| | 20 | | | 25 | | 30 |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Tyr | Tyr | Ala | Tyr | Gln | Arg | Thr | Trp | Lys | Pro | Phe | Asn | Pro | Ile | 35 | 40 | 45 |
| Leu | Gly | Glu | Thr | Tyr | Glu | Met | Val | Asn | His | Gly | Gly | Ile | Thr | Phe | Ile | 50 | 55 | 60 |
| Ser | Glu | Gln | Val | Ser | His | His | Pro | Pro | Met | Ser | Ala | Gly | His | Ala | Glu | 65 | 70 | 75 |
| Thr | Glu | His | Phe | Thr | Tyr | Asp | Val | Thr | Ser | Lys | Leu | Lys | Thr | Lys | Phe | 85 | 90 | 95 |
| Leu | Gly | Asn | Ser | Val | Asp | Val | Tyr | Pro | Val | Gly | Arg | Thr | Arg | Val | Thr | 100 | 105 | 110 |
| Leu | Lys | Arg | Asp | Gly | Val | Val | Leu | Asp | Leu | Val | Pro | Pro | Pro | Thr | Lys | 115 | 120 | 125 |
| Val | Ser | Asn | Leu | Ile | Phe | Gly | Arg | Thr | Trp | Ile | Asp | Ser | Pro | Gly | Glu | 130 | 135 | 140 |
| Met | Ile | Leu | Thr | Asn | Leu | Thr | Thr | Gly | Asp | Lys | Val | Val | Leu | Tyr | Phe | 145 | 150 | 155 |
| Gln | Pro | Cys | Gly | Trp | Phe | Gly | Ala | Gly | Arg | Tyr | Glu | Val | Asp | Gly | Tyr | 165 | 170 | 175 |
| Val | Tyr | Asn | Ser | Ala | Asp | Glu | Pro | Lys | Ile | Leu | Met | Thr | Gly | Lys | Trp | 180 | 185 | 190 |
| Asn | Glu | Ala | Met | Asn | Tyr | Gln | Val | Cys | Asp | Ser | Glu | Gly | Glu | Pro | Leu | 195 | 200 | 205 |
| Pro | Gly | Thr | Glu | Leu | Lys | Glu | Ile | Trp | Arg | Val | Ala | Asp | Thr | Pro | Lys | 210 | 215 | 220 |
| Lys | Asp | Lys | Phe | Gln | Tyr | Thr | His | Phe | Ala | His | Lys | Ile | Asn | Ser | Phe | 225 | 230 | 235 |
| Asp | Thr | Ala | Pro | Lys | Lys | Leu | Leu | Ala | Ser | Asp | Ser | Arg | Leu | Arg | Pro | 245 | 250 | 255 |
| Asp | Arg | Met | Ala | Leu | Glu | Lys | Gly | Asp | Leu | Ser | Thr | Ser | Gly | Tyr | Glu | 260 | 265 | 270 |
| Lys | Ser | Ser | Leu | Glu | Glu | Arg | Gln | Arg | Ala | Glu | Lys | Arg | Asn | Arg | Glu | 275 | 280 | 285 |
| Ala | Lys | Gly | His | Lys | Phe | Thr | Pro | Arg | Trp | Phe | Asp | Leu | Thr | Asp | Glu | 290 | 295 | 300 |
| Val | Thr | Pro | Thr | Pro | Trp | Gly | Asp | Leu | Glu | Val | Tyr | Gln | Tyr | Asn | Gly | 305 | 310 | 315 |
| Lys | Tyr | Thr | Gln | His | Cys | Ala | Ala | Val | Asp | Ser | Ser | Glu | Cys | Ile | Glu | 325 | 330 | 335 |

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Val Pro Asp Ile Arg Pro Glu Phe Asn Pro Trp Gln Tyr Asp Asn Leu
340 345 350

Asp Ala Glu
355

<210> 33
<211> 414
<212> PRT
<213> Zea mays

<400> 33

Met Ala Thr Lys Glu Glu Ala Ser Ala Val Pro Ala Ala Ser Lys Thr
1 5 10 15

Ser Trp Ser Ser Phe Leu Lys Ser Ile Ala Ser Phe Asn Gly Asp Leu
20 25 30

Ser Ser Leu Thr Ala Pro Pro Phe Ile Leu Ser Thr Thr Ser Leu Thr
35 40 45

Glu Tyr Ser Ala Tyr Trp Cys Glu His Pro Ala Leu Phe Val Ala Pro
50 55 60

Ala Arg Glu Pro Asp Pro Ala Lys Arg Ala Leu Leu Val Leu Lys Trp
65 70 75 80

Phe Leu Ser Thr Leu His Gln Gln Tyr Cys Ser Arg Ser Glu Lys Leu
85 90 95

Gly Ser Glu Lys Lys Pro Leu Asn Pro Phe Leu Gly Glu Leu Phe Leu
100 105 110

Gly Lys Trp Ile Glu Asp Glu Asp Val Gly Glu Thr Arg Leu Ile Ser
115 120 125

Glu Gln Val Ser His His Pro Pro Ala Thr Ala Tyr Ser Ile Val Asn
130 135 140

Glu Lys His Gly Val Glu Leu Gln Gly Tyr Asn Ala Gln Lys Ala Ser
145 150 155 160

Phe Ser Ser Thr Ile Gln Val Lys Gln Leu Gly His Ala Tyr Leu Ser
165 170 175

Leu Thr Pro Pro Gly Lys Asp Ala Asn Asn Glu Asp Asp Arg Glu His
180 185 190

Tyr Leu Ile Thr Leu Pro Asn Leu His Ile Glu Ser Leu Ile Tyr Gly
195 200 205

Thr Pro Phe Val Glu Leu Glu Lys Ser Cys Lys Ile Ala Ser Ser Thr
210 215 220

Gly Tyr Ile Ser Lys Ile Asp Phe Ser Gly Lys Gly Trp Leu Ser Gly
 225 230 235 240

Lys Lys Asn Thr Phe Ser Ala Val Leu Tyr Lys Glu Ser Asp Gly Glu
 245 250 255

Lys Asn Pro Leu Tyr Thr Ala Asp Gly Gln Trp Ser Ser Ser Phe Thr
 260 265 270

Ile Arg Asp Ala Arg Ala Lys Lys Asp Ile Glu Thr Phe Thr Ile Ser
 275 280 285

Asn Leu Lys Thr Thr Pro Leu Thr Val Ala Pro Leu Asp Glu Gln Asp
 290 295 300

Glu Trp Glu Thr Arg Arg Ala Trp Arg Asp Val Ala Ala Ala Ile Glu
 305 310 315 320

Arg Gly Asp Met Glu Ala Thr Ser Asn Ala Lys Thr Lys Ile Glu Val
 325 330 335

Ala Gln Arg Glu Leu Arg Lys Lys Glu Lys Glu Gln Gly Glu Glu Trp
 340 345 350

Glu Arg Arg Phe Phe Lys Arg Val Asn Glu Lys Asp Glu Pro Thr Phe
 355 360 365

Met Arg Leu Ala Ala Met Leu Asp Leu Thr Gln Gly Ile Glu Ser Asp
 370 375 380

Arg Thr Gly Gly Val Trp Arg Phe Asp Pro Ser Arg Ala Val Asp Ala
 385 390 395 400

Asn Pro Pro Tyr His Lys Val Gly Gly Glu Gly Leu Gly Leu
 405 410

<210> 34
 <211> 434
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 34

Met Ser Gln His Ala Ser Ser Ser Ser Trp Thr Ser Phe Leu Lys Ser
 1 5 10 15

Ile Ser Ser Phe Asn Gly Asp Leu Ser Ser Leu Ser Ala Pro Pro Phe
 20 25 30

Ile Leu Ser Pro Thr Ser Leu Thr Glu Phe Ser Gln Tyr Trp Ala Glu
 35 40 45

His Pro Ala Leu Phe Leu Glu Pro Ser Leu Ile Asp Gly Glu Asn Tyr
 50 55 60

Lys Asp His Cys Pro Phe Asp Pro Asn Val Glu Ser Lys Glu Val Ala

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10030537 042300

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| 65 | | 70 | | 75 | | 80 |
| Gln Met Leu Ala Val Val Arg Trp Phe Ile Ser Thr Leu Arg Ser Gln | | | | | | |
| | | 85 | | 90 | | 95 |
| Tyr Cys Ser Arg Ser Glu Ser Met Gly Ser Glu Lys Lys Pro Leu Asn | | | | | | |
| | | 100 | | 105 | | 110 |
| Pro Phe Leu Gly Glu Val Phe Val Gly Lys Trp Lys Asn Asp Glu His | | | | | | |
| | | 115 | | 120 | | 125 |
| Pro Glu Phe Gly Glu Thr Val Leu Leu Ser Glu Gln Val Ser His His | | | | | | |
| | | 130 | | 135 | | 140 |
| Pro Pro Met Thr Ala Phe Ser Ile Phe Asn Glu Lys Asn Asp Val Ser | | | | | | |
| | | 145 | | 150 | | 155 |
| Val Gln Gly Tyr Asn Gln Ile Lys Thr Gly Phe Thr Lys Thr Leu Thr | | | | | | |
| | | 165 | | 170 | | 175 |
| Leu Thr Val Lys Pro Tyr Gly His Val Ile Leu Lys Ile Lys Asp Glu | | | | | | |
| | | 180 | | 185 | | 190 |
| Thr Tyr Leu Ile Thr Thr Pro Pro Leu His Ile Glu Gly Ile Leu Val | | | | | | |
| | | 195 | | 200 | | 205 |
| Ala Ser Pro Phe Val Glu Leu Gly Gly Arg Ser Phe Ile Gln Ser Ser | | | | | | |
| | | 210 | | 215 | | 220 |
| Asn Gly Met Leu Cys Val Ile Glu Phe Ser Gly Arg Gly Tyr Phe Thr | | | | | | |
| | | 225 | | 230 | | 235 |
| Gly Lys Lys Asn Ser Phe Lys Ala Arg Ile Tyr Arg Ser Pro Gln Glu | | | | | | |
| | | 245 | | 250 | | 255 |
| His Ser His Lys Glu Asn Ala Leu Tyr Leu Ile Ser Gly Gln Trp Ser | | | | | | |
| | | 260 | | 265 | | 270 |
| Gly Val Ser Thr Ile Ile Lys Lys Asp Ser Gln Val Ser His Gln Phe | | | | | | |
| | | 275 | | 280 | | 285 |
| Tyr Asp Ser Ser Glu Thr Pro Thr Glu His Leu Leu Val Lys Pro Ile | | | | | | |
| | | 290 | | 295 | | 300 |
| Glu Glu Gln His Pro Leu Glu Ser Arg Arg Ala Trp Lys Asp Val Ala | | | | | | |
| | | 305 | | 310 | | 315 |
| Glu Ala Ile Arg Gln Gly Asn Ile Ser Met Ile Lys Lys Thr Lys Glu | | | | | | |
| | | 325 | | 330 | | 335 |
| Glu Leu Glu Asn Lys Gln Arg Ala Leu Arg Glu Gln Glu Arg Val Lys | | | | | | |
| | | 340 | | 345 | | 350 |
| Gly Val Glu Trp Gln Arg Arg Trp Phe Lys Gln Val Asp Tyr Met Asn | | | | | | |
| | | 355 | | 360 | | 365 |
| Glu Asn Thr Ser Asn Asp Val Glu Lys Ala Ser Glu Asp Asp Ala Phe | | | | | | |

380

Thr Ile

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